

# **EXHIBIT A**

파일(F) 편집(E) 보기(V) 즐겨찾기(A) 도구(T) 도움말(H)



주소(ⓐ) <http://www.uniprot.org/uniprot/P12643>

## Sequences

### Sequence

☐ P12643-1 [UniParc].

Last modified October 1, 1989, Version 1.

Checksum: 20653A3987B25E60

Length Mass (Da) Tools

FASTA 396 44,702

Blast

→ BMP-2 sequence (283-396)

→ 1-282 : Signal peptide + Propeptide  
gp

→ SEQ ID No:3 of the present invention:  
2-18 of the above BMP-2 (red underline) : 17 amino acids

→ SEQ ID No:6 of the present invention:  
24-40 of the above BMP-2 (pink underline) : 17 amino acids

• SEQ ID No: 10 of the present invention:  
283-302 of BMP- 2 precursor (violet underline)

• SEQ ID No: 11 of the present invention:  
355-374 of BMP-2 precursor (green underline)

• SEQ ID No: 12 of the present invention:  
370-390 of BMP-2 precursor (yellow underline)

10 20 30 40 50 60  
MVAGTRCLLA LLLPQVLLGG AAGLVPELGR RKFAAASSGR PSSQPSDEVL SEFELRLLSM

70 80 90 100 110 120  
FGLKQRPTPS RDAVVPYML DLYRRHSGQP GSPAPDHRLE RAASRANTVR SFHHEESLEE

130 140 150 160 170 180  
LPETSGKTTR RFFFNLSIP TEEFITSAEL QVFREQMQDA LGNSSFHHR INIYEIIKPA




190 200 210 220 230 240  
TANSKFPVTR LLDTRLVNQW ASRWESFDVT PAVMRWTAQG HANHGFFVEV AHLEEKQGVV

250 260 270 280 290 300  
KRHVRIISRL HODEHSWSQI RPLLVTFGHD GKGHPLHKRE KROAKHKQRK RLKSSCKRHP

310 320 330 340 350 360  
LYVDFSDVGV NDUIVAPPGY HAFYCHGECF PPLADHLNST NHAIVQTLVN SYNSKIPKAC

370 380 390  
CVPTELSAIS MLYLDENEKV VLKNYODMWV EGGCGCR

# TOBACCO

Feature key	Position(s)	Length	Description	Graphical view	Feature identifier
<b>Molecule processing</b>					
<input type="checkbox"/> Signal peptide	1 – 23	23	Potential		
<input type="checkbox"/> Propeptide	24 – 282	259			PRO_0000033824
<input type="checkbox"/> Chain	283 – 396	114	Bone morphogenetic protein 2		PRO_0000033825

### Amino acid modifications

<input type="checkbox"/>	Glycosylation	135	1	N-linked (GlcNAc...)	Potential	
<input type="checkbox"/>	Glycosylation	163	1	N-linked (GlcNAc...)	Potential	
<input type="checkbox"/>	Glycosylation	164	1	N-linked (GlcNAc...)	Potential	
<input type="checkbox"/>	Glycosylation	200	1	N-linked (GlcNAc...)	Potential	
<input type="checkbox"/>	Disulfide bond	296 ↔ 361				
<input type="checkbox"/>	Disulfide bond	325 ↔ 393				
<input type="checkbox"/>	Disulfide bond	329 ↔ 395				
<input type="checkbox"/>	Disulfide bond	360		Interchain		

# **EXHIBIT B**

편집(드) 보기(이) 즐겨찾기(아) 도구(이) 도움말(나)



http://www.uniprot.org/uniprot/P12644

Last modified October 1, 1989. Version 1.  
Checksum: 79B01179DBB98204

- BMP-4 sequence (293~408).
- 1~292 : Signal peptide + Propeptide
- SEQ ID No: 4 of the present invention : 2-18 of the above BMP-4 (red underline) : 17 amino acids

10	20	30	40	50	60
NIPGNRMLNV	VLLCQVLLGG	ASHASLIPET	GKKKVAEIQG	HAGGRRSGQS	HELLRDPEAT
70	80	90	100	110	120
LLQMFGLRRR	POPSKSAVIP	DYMRDLVRLQ	SGEEEEQIH	STGLEYPERP	ASRANTVRSF
130	140	150	160	170	180
HHEEHLENIP	GTSSENSAFRF	LFNLSSIPEN	EVISSAELRL	FREQVDQGPD	WERGFHRINI
190	200	210	220	230	240
YEVMPKPPAEV	VPGHLITRLL	DTRLVHHNVT	RWETFDVSPA	VLRWTREKQP	NYGLAIEVTH
250	260	270	280	290	300
LHQTRTHQGG	HVRISRLPQ	GSGNWAQLRP	LLVTFGHDGR	GHALTRRRRA	KREFVHHSQD
310	320	330	340	350	360
ARVKKHAKGRR	HSLVWDFSDV	GWNDWIVAPP	GYQAFYCHGD	CPFFPLADHLN	STNHAIIVQTL
370	380	390	400		
VNSVNSSIRK	AGCVPTLSA	ISHLYLDEYD	KVVLKNYOEM	VVEGCGCR	

• SEQ ID No: 14 of the present invention:  
293-313 of BMP-4 precursor (violet underline)

• SEQ ID No: 15 of the present invention:  
366-386 of BMP-4 precursor (green underline)

• SEQ ID No: 16 of the present invention:  
382-402 of BMP-4 precursor (yellow underline)

« Hide

References

« Hide 'large scale' references

파일(F) 편집(E) 보기(V) 즐겨찾기(A) 도구(T) 도움말(H)



주소(1) <http://www.uniprot.org/uniprot/P12644>

### Sequence annotation [Features]

Feature key	Position(s)	Length	Description	Graphical view	F
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#### Molecule processing

<input type="checkbox"/>	Signal peptide	1 – 19	19	Potential		
<input type="checkbox"/>	Propeptide	20 – 292	273			F
<input type="checkbox"/>	Chain	293 – 408	116	Bone morphogenetic protein 4		F

#### Amino acid modifications

<input type="checkbox"/>	Glycosylation	143	1	N-linked (GlcNAc...)	Potential	
<input type="checkbox"/>	Glycosylation	208	1	N-linked (GlcNAc...)	Potential	
<input type="checkbox"/>	Glycosylation	350	1	N-linked (GlcNAc...)	Potential	
<input type="checkbox"/>	Glycosylation	365	1	N-linked (GlcNAc...)	Potential	
<input type="checkbox"/>	Disulfide bond	308 ↔ 373		By similarity		
<input type="checkbox"/>	Disulfide bond	337 ↔ 405		By similarity		
<input type="checkbox"/>	Disulfide bond	341 ↔ 407		By similarity		
<input type="checkbox"/>	Disulfide bond	372		Interchain	By similarity	

# **EXHIBIT C**

THE NEW YORK PUBLIC LIBRARY

## Sequence

☐ P22004-1 [UniParc].

FASTA 513 57.226

Length      Mass (Da)      Tools

# Best

Last modified August 1, 1991. Version 1.

Checksum: 3F19155B36049278

	10	20	30	40	50	60
MPGLGRRAGM	LCNNHGLICS	CCGPPPIPPP	LPAAAAAG	CGTICGCGSP	GGTTCGGGSP	

QSSSGFLYRR LKTOEKREMQ KEILSVLGLP HRPRLHGLQ QPQPPALRQQ QPQPPALRQQ EEQQQQQQLP

13Q 14Q 15Q 16Q 17Q 18Q  
RGEPPPGRLK SAPLFMLDLY NALSADNDED GASEGERQQS WPHEAASSSQ RRQPPPPGAHH

190 PLNRKSLAP GSGSGGASPL TSAQDSAFLN DADNVMSFN LVEYDKFSP RORHHKEFKF  
200 210 220 230 240

NLSQIPEGEV VTAAEFRIYK DCVMGSEFKNQ TFLISYQVL QEEHQHSDSL FLLDTRVWMA 250 260 270 280 290 300

310 SEEUGLEFDI TATSNLWVVT PQHNGLQLS VVTRDGVHVH PRAAGLVGRD GPYDKOPFWV  
320 330 340 350 360

370	380	390	400	410	420
AFFKVSEVHV	RTTRBASSRR	ROQSRNRSTQ	SQDVARVSSA	SDYNSSSELEK	ACRKHHELYWS

FQDLGWQDWI	43Q	44Q	45Q	46Q	47Q	48Q
IAPKGYAANY		CDGECSFPLN	AHMNATNHAI	VQTLVHLMNP	FVYKPKPECCAP	

TKLNAISVL<sup>Y</sup> FDDNSNVILK KYRNNVVRAC GCH

epit

100%  
 90%  
 80%  
 70%  
 60%  
 50%  
 40%  
 30%  
 20%  
 10%  
 0%

→ BMP-6 sequence (375~513)  
→ 1~374: Signal peptide + Propeptide

→ SEQ ID No: 5 of the present invention:  
2-18 of the above BMP-6 (red underline):  
17 amino acids

•SEQ ID No: 18 of the present invention:  
397-418 of BMP-6 precursor (violet  
underline)

• SEQ ID No: 19 of the present invention:  
472-490 of BMP-6 precursor (green  
underline)

• SEQ ID No: 20 of the present invention:  
487-510 of BMP-6 precursor (yellow  
underline)



파일(F) 편집(E) 보기(V) 즐겨찾기(A) 도구(T) 도움말(H)



주소(U) <http://www.uniprot.org/uniprot/P22004>

## Sequence annotation (Features)

Feature key	Position(s)	Length	Description	Graphical view
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### Molecule processing

<input type="checkbox"/> Signal peptide	1 – 20	20	Potential	
<input type="checkbox"/> Propeptide	21 – 374	354	Potential	
<input type="checkbox"/> Chain	375 – 513	139	Bone morphogenetic protein 6	

### Amino acid modifications

<input type="checkbox"/> Glycosylation	241	1	N-linked (GlcNAc...)	Potential	
<input type="checkbox"/> Glycosylation	269	1	N-linked (GlcNAc...)	Potential	
<input type="checkbox"/> Glycosylation	386	1	N-linked (GlcNAc...)	Potential	
<input type="checkbox"/> Glycosylation	404	1	N-linked (GlcNAc...)	Potential	
<input type="checkbox"/> Glycosylation	454	1	N-linked (GlcNAc...)	Potential	
<input type="checkbox"/> Disulfide bond	412 ↔ 478		By similarity		
<input type="checkbox"/> Disulfide bond	441 ↔ 510		By similarity		
<input type="checkbox"/> Disulfide bond	445 ↔ 512		By similarity		
<input type="checkbox"/> Disulfide bond	477		Interchain	By similarity	

### Natural variations

<input type="checkbox"/> Natural variant	257	1	R → C: dbSNP rs10458105		
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# **EXHIBIT D**

파일(F) 편집(E) 보기(V) 즐겨찾기(A) 도구(T) 도움말(H)



주소(1) <http://www.uniprot.org/uniprot/P18075&format=html>

Details...

## Sequences

### Sequence

☐ P18075-1 [UniParc].

Last modified November 1, 1990, Version 1.

Checksum: 47A05E45C6815F8A

### Length Mass (Da) Tools

FASTA 431 49,313

→ BMP-7 sequence (293~431)

→ 1~292: Signal peptide + Propeptide

→ SEQ ID No: 21 of the present invention:  
98-117 of BMP-7 (pink underline)

(The above sequence is equal to SEQ ID  
No: 23 of the present invention (390-409 of  
BMP-7 precursor.)

• SEQ ID No: 22 of the present invention:  
320-340 of BMP-7 precursor (violet  
underline)

• SEQ ID No: 24 of the present invention:  
405-423 of BMP-7 precursor (red underline)

10 MHVSLRAAA PHSFVALWAP LFLRLRSALAD FSLDNEVHSS FIHRLRSQE RREMQREILS 60

70 ILGLPHRRP HLOQKENSAP MFMLDLYNAM AVEEGGGPGG QGFSYPYKAV FSTQGPPLAS 120

130 LQDSHPLTDA DMVNSFVNIV EHDKEFFHPR YHHRFRFDL SKIPEGEAVT AAEFRYKYD 180

190 IRERFDNETF RISVYQVLQE HLGRESDLFL LDSRTLWASE EGWLVDITA TSNHVVVNPR 240




250 HNLGLQLSVE TLDGQSINPK LAGLIGHGP QNKQPFMVAF FKATEVHFRS INSTGSKQRS 300

310 QNRSKTPKNQ EALRMANVAE NSSSDQRQAC KKHELYVSFR DLGWQDWIIA PEGYAAAYCE 360

370 GFCAPPLNSY MNAITHAIVQ TLVHFINPET VPKPCCAPTQ LNAISVLYFD DSSNVILKKY 420

430 RNWVVRACGC H

# STANLEY

Feature key	Position(s)	Length	Description	Graphical view	Feature identifier
<b>Protein processing</b>					
Signal peptide	1 – 29	29	Potential		
Propeptide	30 – 292	263	Ref.5		PRO_0000033876
Chain	293 – 431	139	Bone morphogenetic protein 7		PRO_0000033877

### Amino acid modifications

<input type="checkbox"/>	Glycosylation	187	1	N-linked (GlcNAc...)	Potential
<input type="checkbox"/>	Glycosylation	302	1	N-linked (GlcNAc...)	Potential
<input type="checkbox"/>	Glycosylation	321	1	N-linked (GlcNAc...)	Potential
<input type="checkbox"/>	Glycosylation	372	1	N-linked (GlcNAc...)	Potential

## Secondary structure

# **EXHIBIT E**

## **Partial translation for KR 10-2004-0019010**

**Page 7 /27**

### **[Disclosure of invention]**

<15> To achieve the above object, the present invention provides a barrier membrane and a implant which have a cell adhesion-inducing peptide and/or tissue growth factor-derived peptide immobilized on the surface of the membrane or the implant bonded with a cross-linking agent.

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**Page 8 / 27**

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<19> Specifically, the cell adhesion-inducing peptide is preferably a peptide having an amino acid sequence of SED ID NO: 1. More preferably, it is an amino acid sequence of SEQ ID NO: 2 or an amino acid sequence of SEQ ID NO: 3 designed to maintain the structural stability of the amino acid sequence of SEQ ID NO: 1, RGD. Furthermore, the tissue growth factor-derived peptide is a peptide identified and chemically synthesized from the active site of the tissue growth factor. Preferably it is at least one peptide selected from the group consisting of the following peptides:

<20> (a) the amino acid sequence at positions 283-302 (SEQ ID NO: 4), the amino acid sequence at positions 335-353 (SEQ ID NO: 5) and the amino acid sequence at positions 370-390 (SEQ ID NO: 6) of bone morphogenetic proteins (BMP)-2;

<21> the amino acid sequence at positions 293-313 (SEQ ID NO: 7), the amino acid sequence at positions 360-379 (SEQ ID NO: 8) and the amino acid sequence at positions 382-402 (SEQ ID NO: 9) of BMP-4;

<22> the amino acid sequence at positions 397-418 (SEQ ID NO: 10), the amino

acid sequence at positions 472-490 (SEQ ID NO: 11) and the amino acid sequence at positions 487-510 (SEQ ID NO: 12) of BMP-6;

<23> the amino acid sequence at positions 320-340 (SEQ ID NO: 13), the amino acid sequence at positions 390-409 (SEQ ID NO: 14) and the amino acid sequence at positions 405-423 (SEQ ID NO: 15) of BMP-7;

**Page 9 /27**

<24> (b) the amino acid sequence at positions 199-204 (SEQ ID NO: 16), the amino acid sequence at positions 151-158 (SEQ ID NO: 17), the amino acid sequence at positions 275-291 (SEQ ID NO: 18), the amino acid sequence at positions 20-28 (SEQ ID NO: 19), the amino acid sequence at positions 65-90 (SEQ ID NO: 20), the amino acid sequence at positions 150-170 (SEQ ID NO: 21) and the amino acid sequence at positions 280-290 (SEQ ID NO: 22) of bone sialoprotein,

<25> (c) the amino acid sequence at positions 242-250 (SEQ ID NO: 23), the amino acid sequence at positions 279-299 (SEQ ID NO: 24) and the amino acid sequence at positions 343-361 (SEQ ID NO: 25) of a transforming growth factor beta 1,

<26> (d) the amino acid sequence at positions 100-120 (SEQ ID NO: 26) and the amino acid sequence at positions 121-140 (SEQ ID NO: 27) of a platelet-derived growth factor,

<27> (e) the amino acid sequence at positions 23-31 (SEQ ID NO: 28) and the amino acid sequence at positions 97-105 (SEQ ID NO: 29) of an acidic fibroblast growth factor,

<28> (f) the amino acid sequence at positions 16-27 (SEQ ID NO: 30), the amino acid sequence at positions 37-42 (SEQ ID NO: 31), the amino acid sequence at positions

78-84 (SEQ ID NO: 32) and the amino acid sequence at positions 107-112 (SEQ ID NO: 33) of a basic fibroblast growth factor,

<29> (g) the amino acid sequence at positions 255-275 (SEQ ID NO: 34), the amino acid sequence at positions 475-494 (SEQ ID NO: 35) and the amino acid sequence at positions 551-573 (SEQ ID NO: 36) of dentin sialoprotein,

<30> (h) the amino acid sequence at positions 63-83 (SEQ ID NO: 37), the amino acid sequence at positions 84-103 (SEQ ID NO: 38), the amino acid sequence at positions 104-116 (SEQ ID NO: 39) and the amino acid sequence at positions 121-140 (SEQ ID NO: 40) of a heparin binding EGF-like growth factor,

**Page 10 / 27**

<31> (i) the amino acid sequence at positions 326-350 (SEQ ID NO: 41), the amino acid sequence at positions 351-371 (SEQ ID NO: 42), the amino acid sequence at positions 372-400 (SEQ ID NO: 43), the amino acid sequence at positions 401-423 (SEQ ID NO: 44), the amino acid sequence at positions 434-545 (SEQ ID NO: 45), the amino acid sequence at positions 546-651 (SEQ ID NO: 46), the amino acid sequence at positions 1375-1433 (SEQ ID NO: 47), the amino acid sequence at positions 1435-1471 (SEQ ID NO: 48), the amino acid sequence at positions 1475-1514 (SEQ ID NO: 49), the amino acid sequence at positions 1515-1719 (SEQ ID NO: 50), the amino acid sequence at positions 1764-1944 (SEQ ID NO: 51) and the amino acid sequence at positions 2096-2529 (SEQ ID NO: 52) of the cadherin EGF LAG seven-pass G-type receptor 3,

<32> (j) the amino acid sequence at positions 54-159 (SEQ ID NO: 53), the amino acid sequence at positions 160-268 (SEQ ID NO: 54), the amino acid sequence at positions 269-383 (SEQ ID NO: 55), the amino acid sequence at positions 384-486



(SEQ ID NO: 56) and the amino acid sequence at positions 487-612 (SEQ ID NO: 57) of an osteoblast specific cadherin (OB-cadherin).

<33> The N-terminal end of the peptide has an addition of cysteine and two glycines so as to stabilize the structure of the peptide and to facilitate chemical immobilization of the peptide to the barrier membrane.

**Page 11 / 27**

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<35> As the barrier membrane to be surface-activated by the present invention, all kinds and types of barrier membranes can be used if they are used in the technical field. Preferred examples of these barrier membranes include porous membranes made of polylactic acid, regeneration membranes made of nanofibers of chitin or chitosan, and film-shaped barrier membranes made of chitin or chitosan. Also, as the implants, titanium implants are preferably used but are not limited thereto. In this respect, the surface of the implants is preferably modified by oxidation and nitrification so as to facilitate the adhesion of the active peptide to the surface.

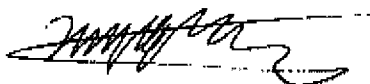
# VERIFICATION OF TRANSLATION

I, BAE, Young Sim of 11<sup>th</sup> Yeosam Bldg., 648-23, Yeoksam-dong,  
Gangnam-gu, Seoul, 135-080, Republic of Korea

State that the attached document is a true and accurate translation of  
Korean Patent Application No. 10-2004-0019010 in Korean (language of  
original specification) to the best of my knowledge and belief.

Dated this August 3, 2009

Signature of Translator:

A handwritten signature in black ink, appearing to read 'BAE, Young Sim', written over a horizontal line.